Figure 1A

```
1   ACAAATGACCGGGAGCCATGACGTCATCGGGGGCGCAGGAAAGCAGGTGCTCTGCTGCTT   60
1       M  T  G  S  H  D  V  I  G  G  A  G  K  Q  V  L  C  C  F   19

61  TTGCAAGCAGAGAAATAAGAGTTTGGGCACCTACCCAGGGGTCCCAGGGAATGCCCTGTG  120
20  C  K  Q  R  N  K  S  L  G  T  Y  P  G  V  P  G  N  A  L  C   39

121 GCTCCTGACCTCCCCCGCCTGTAATGCTCTGAGCACTTCAGCAGTAATGCATGGAAGAGA  180
40  L  L  T  S  P  A  C  N  A  L  S  T  S  A  V  M  H  G  R  D   59

181 TAAGGGGTCTGTGACCCATGGAACTGTCCAAGTCCTCTCTGACACCCGCTTCTTTTCCTG  240
60  K  G  S  V  T  H  G  T  V  Q  V  L  S  D  T  R  F  F  S  C   79

241 CCGTGAAGGACTACTTCCAGCAACCCAGTCTCCTGCCATGTCCGACCCCATCACGCTGAA  300
80  R  E  G  L  L  P  A  T  Q  S  P  A  M  S  D  P  I  T  L  N   99

301 CGTCGGGGGGAAGCTCTATACAACCTCACTGGCGACCCTGACCAGCTTCCCTGACTCCAT  360
100 V  G  G  K  L  Y  T  T  S  L  A  T  L  T  S  F  P  D  S  M   119

361 GCTAGGCGCCATGTTCAGCGGGAAGATGCCCACCAAGAGGGACAGCCAGGGCAACTGCTT  420
120 L  G  A  M  F  S  G  K  M  P  T  K  R  D  S  Q  G  N  C  F   139

421 CATTGACCGTGACGGCAAAGTGTTCCGCTATATCCTCAACTTCCTGCGGACCTCCCACCT  480
140 I  D  R  D  G  K  V  F  R  Y  I  L  N  F  L  R  T  S  H  L   159

481 TGACCTGCCTGAGGACTTCCAGGAGATGGGGCTGCTCCGCAGGGAGGCCGACTTCTACCA  540
160 D  L  P  E  D  F  Q  E  M  G  L  L  R  R  E  A  D  F  Y  Q   179

541 GGTGCAGCCCCTGATTGAGGCCCTGCAGGAGAAGGAAGTGGAGCTCTCCAAGGCCGAGAA  600
180 V  Q  P  L  I  E  A  L  Q  E  K  E  V  E  L  S  K  A  E  K   199

601 GAATGCCATGCTCAACATCACACTGAACCAGCGTGTGCAGACGGTCCACTTCACTGTGCG  660
200 N  A  M  L  N  I  T  L  N  Q  R  V  Q  T  V  H  F  T  V  R   219

661 CGAGGCACCCCAGATCTACAGCCTCTCCTCTTCCAGCATGGAGGTCTTCAACGCCAACAT  720
220 E  A  P  Q  I  Y  S  L  S  S  S  S  M  E  V  F  N  A  N  I   239

721 CTTCAGCACCTCCTGCCTCTTCCTCAAGCTCCTTGGCTCTAAGCTCTTCTACTGCTCCAA  780
240 F  S  T  S  C  L  F  L  K  L  L  G  S  K  L  F  Y  C  S  N   259

781 TGGCAATCTCTCCTCCATCACCAGCCACTTGCAGGACCCCAACCACCTGACTCTGGACTG  840
260 G  N  L  S  S  I  T  S  H  L  Q  D  P  N  H  L  T  L  D  W   279

841 GGTGGCCAATGTGGAGGGCCTGCCAGAGGAGGAGTACACCAAGCAGAACCTCAAGAGGCT  900
280 V  A  N  V  E  G  L  P  E  E  E  Y  T  K  Q  N  L  K  R  L   299
```

Figure 1B

```
901  CTGGGTGGTGCCCGCCAACAAGCAGATCAACAGCTTCCAGGTCTTCGTGGAAGAGGTACT  960
300   W  V  V  P  A  N  K  Q  I  N  S  F  Q  V  F  V  E  E  V  L   319

961  GAAAATCGCTCTGAGCGATGGCTTCTGCATCGATTCTTCTCACCCACATGCTCTGGATTT  1020
320   K  I  A  L  S  D  G  F  C  I  D  S  S  H  P  H  A  L  D  F   339

1021 TATGAACAATAAGATTATTCGATTAATACGGTACAGGTAAAAGGACCCCAACAACACTGG  1080
340   M  N  N  K  I  I  R  L  I  R  Y  R                          351

1081 AGATGGGGAGTCCCAGGAAGCTCATGTCAGCCAGGTCTTGGAGGGCATCTCGCCAGTGGT  1140

1141 GCGAGGCAGGGGACTATACTAATCTGTATTAATTGTGTAGCAGGACTTGATTCCCCCCAT  1200

1201 GATGAAGTCCACCTTTTGGAATCCAGTGTCCTCTGAACAGAACCACCTTTTTTCTTGCCA  1260

1261 TTTTGAGCTGCAGACAGGCGGTTTATTATGACAAGTGAAGAGTCAGCTGATGTGTACTAA  1320

1321 AGGAGGCCATAGGAGGATTTTCCAGCCAGGACAAAAGAGCAGCAGTTTTCTCCTGGGCTC  1380

1381 CATCTCTCTGTACCGCTAGCCAGTGCCGCATTTATCCATCTGTAAGAAGGCCCTGGTGGA  1440

1441 GAGGATGGGATGAGAACAAGAGGCTACCTCCAGTTAACCAGGACATAAAGTCCCCAGCGG  1500

1501 TTCCTGTCACACCTGCTCCTCCCTCCCCAGGGTGCATCCATGATCGTGGATGTTTGCCCA  1560

1561 GGGGTGACCATGTTTGGCTGGCTTGGAATGCTGTGCATTCTCAGAGCTCTGTTAGTGTCC  1620

1621 CCTCTTGGGGGTCAGAGATGAGGTGTGGCAGGGTCTAGAGGAATGAGTGTCCAGGCAGAG  1680

1681 TTCAGAAGGTAGGAATGTCCCTCTTGATAGGGCTGAATCAAGGGATTCCTGGCTTTAGAA  1740

1741 AGGGTCTGCTATCTTTGCAAAAATGTGCAAGTATCTGTAGCCAGTGTAATGAAATCACTT  1800

1801 CCAAATCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  1839
```

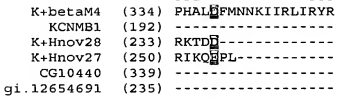
D0115 NP

Figure 2A

```
                       1                                                50
    K+betaM4    (1)    --------MTGSHDVIGGAGKQVLCCFCKQRNKSLGTYPGVPGNALWLLT
      KCNMB1    (1)    --------------------------------------------------
    K+Hnov28    (1)    --------------------------------------------------
    K+Hnov27    (1)    --------------------------------------------------
     CG10440    (1)    MDRERERDVKALEPRDLSSTGRIYARSDIKISSSPTVSPTISNSSSPTPT
 gi.12654691    (1)    --------------------------------------------------

                       51                                              100
    K+betaM4   (43)    SPACNALSTSAVMHGRDKGSVTHG----TVQVLSDTRFFSCREGLLPATQ
      KCNMB1    (1)    --------------------------------MVKKLVMAQKRGETRALC
    K+Hnov28    (1)    --------------------------------------------MDNGDW
    K+Hnov27    (1)    --------------------------MSRPLITRSPASPLXNQGIPTPAQ
     CG10440   (51)    PPASSSVTPLGLPGAVAAAAAAVGGASSAGASSYLHGNHKPITGIPCVAA
 gi.12654691    (1)    MPHRKERPSGSSLHTHGSTGTAEGGNMSRLSLTRSPVSPLAAQGIPLPAQ

                       101                                             150
    K+betaM4   (89)    SPAMSDPITLNVGGKLYTTSLATLTSFPDSMLGAMFSGKMPTKRDSQ-GN
      KCNMB1   (19)    LGVTMVVCAVITYYILVTTVLPLYQKSVWTQESKCHLIETNIRDQEELKG
    K+Hnov28    (7)    GYMMTDPVTLNVGGHLYTTSLTTLTRYPDSMLGAMFGGDFPTARDFQ-GN
    K+Hnov27   (25)    LTKSNAPVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQH
     CG10440  (101)    ASRYTAPVHIDVGGTIYTSSLETLTKYPESKLAKLFNGQIPIVLDSLKQH
 gi.12654691   (51)    LTKSNAPVHIDVGSHMYTSSLATLTKYPDSRISRLFNGTEPIVLDSLKQH

                       151                                             200
    K+betaM4  (138)    CFIDRDGKVFRYILNFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEAL
      KCNMB1   (69)    KKVPQYPCLWVNVSAAGRWAVLYHTEDTRDQNQQCSYIPGSVDNYQTARA
    K+Hnov28   (56)    YFIDRDGPLFRYVLNFLRTSELTLPLDFKEEDLLRKEADFYQIEPLIQCL
    K+Hnov27   (75)    YFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPMLLEM
     CG10440  (151)    YFIDRDGGMFRHILNFMRNSRLLIAEDFPDLELLLEEARYYEVEPMIKQL
 gi.12654691  (101)    YFIDRDGEIFRYVLSFLRTSKLLLPDDFKDFSLLYEEARYYQLQPMVREL

                       201                                             250
    K+betaM4  (188)    QEKEVELSKAEKNAMLNITLNQRVQTVHFTVREAPQIYS---LSSSSMEV
      KCNMB1  (119)    DVEKVRAKFQ--------------------EQQVFYCFS---APRGNETS
    K+Hnov28  (106)    NDPKPLYPMD-------------------TFEEVVELS----STRKLSKY
    K+Hnov27  (125)    ERWKQDRETG-------------------RFSRPCEC----LVVRVAPDL
     CG10440  (201)    ESMRKDRVRNGNYLVAPPTPPARHIKTSPRTSASPECNYEVVALHISPDL
 gi.12654691  (151)    ERWQQEQEQR-------------------RRSRACDC----LVVRVTPDL

                       251                                             300
    K+betaM4  (235)    FNANIFSTSCLFLKLLGSKLFYCSNGNLSSITSHLQDPNHITLDWVANVE
      KCNMB1  (146)    VLFQRLYGPQALLFSLFWPTFLLTGGLLIIAMVKSNQYLSILAAQK----
    K+Hnov28  (133)    SNPVAVIITQLTITTKVHSLLEGISNYFTKWNKHMMDTRDCQVSFTFGPC
    K+Hnov27  (152)    GERITLSGDKSLIEEVFPEIGDVMCNSVN-AGWNH-DSTHVIRFPLNGYC
     CG10440  (251)    GERIMLSAERALLDELFPEASQATQSSRSGVSWNQGDWGQIIRFPLNGYC
 gi.12654691  (178)    GERIALSGEKALIEEVFPETGDVMCNSVN-AGWNQ-DPTHVIRFPLNGYC

                       301                                             350
    K+betaM4  (285)    GLPEEEYTKQNLKRLWVVPANKQIN-SFQVFVEEVLKIALSDGFCIDSSH
      KCNMB1  (192)    --------------------------------------------------
    K+Hnov28  (183)    DYHQEVSLRVHLMEYITKQGFTIRNTRVHHMSERANENTVEHNWTFCRLA
    K+Hnov27  (200)    HLNSVQVLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI
     CG10440  (301)    KLNSVQVLTRLLNAGFTIEASVGG----QQFSEYLLARRVPM--------
 gi.12654691  (226)    RLNSVQDVL-----------------------------------------
```

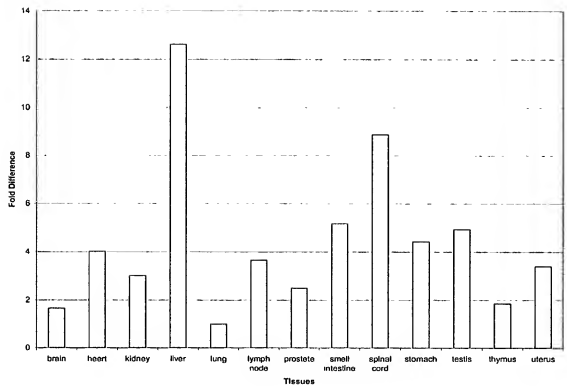
D0115 NP

Figure 2B



D0115 NP

Figure 3



D0115 NP

Figure 4.

K+betaM4

Protein	Genbank ID	Identities	Similarities
human potassium channel K+Hnov27 protein	gi| Y34125	31.6%	45.1%
human potassium channel K+Hnov28 protein	gi| Y34129	42.3%	50.5%
human neuroblastoma protein	gi|12654691	36.2%	47.3%
Drosophila CG10440 protein	gi|7291303	28.0%	38.6%
Human Maxi-K potassium channel beta subunit, KCNMB1	gi|4758625	26.1%	39.1%

K+betaM5

Protein	Genbank ID	Identities	Similarities
human potassium channel K+Hnov28 protein	gi| Y34129	31.7%	43.4%
the human lung protein, MGC:2376	gi|12654469	34.4%	45.6%
human MSTP028 protein	gi|11640564	31.7%	43.4%
Caenorhabditis K+ channel tetramerisation domain containing protein	gi|3875362	34.4%	45.6%
Drosophila CG10465 protein	gi|7302243	30.8%	38.3%
Human Maxi-K potassium channel beta subunit, KCNMB1	gi|4758625	20.0%	40.0%

D0115 NP

Figure 5

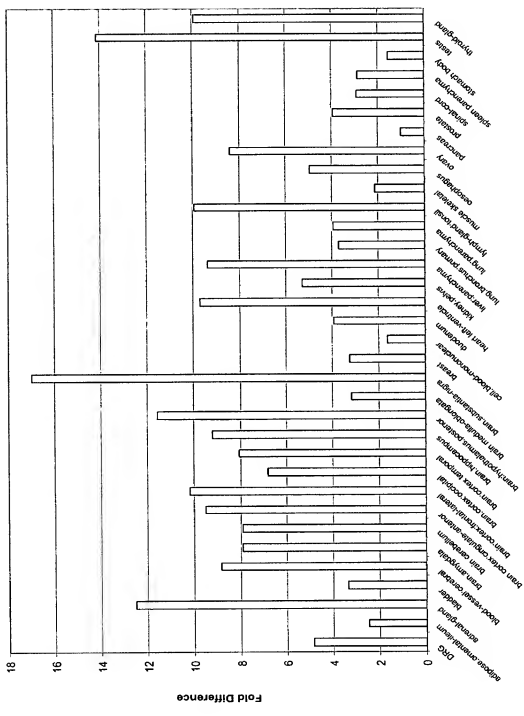


Figure 6A

```
  1 ATGACGATGGCGGTTTTGCGGAATAGAAAAGGGGGAAAGGGACCACTCAGGCGCCGGCCG   60
  1 M  T  M  A  V  L  R  N  R  K  G  G  K  G  P  L  R  R  R  P    20

 61 CTGGCGCTGCCTGCTCTTCGACTGGGCGAGCTTCCTGCCAATCAGGGCGGAACCAGCGCG  120
 21 L  A  L  P  A  L  R  L  G  E  L  P  A  N  Q  G  G  T  S  A    40

121 GCGTCGGCCAGTAGCGGGAGGCGGTCGGGTCAGGCCCCAGCTGGGCGCGAGCGGGTCGGC  180
 41 A  S  A  S  S  G  R  R  S  G  Q  A  P  A  G  R  E  R  V  G    60

181 GTTGAGGGAGCCACCGCCCTCCCGCCTGCGCACTGCCTCTCGCCCCCCTCCGGCCAGCCC  240
 61 V  E  G  A  T  A  L  P  P  A  H  C  L  S  P  P  S  G  Q  P    80

241 GCAGCCGGCCGCGTCATGCCAGGCGCTGCTCGGCGAGCCAGAGGGATGGTGGTAGTCACG  300
 81 A  A  G  R  V  M  P  G  A  A  R  R  A  R  G  M  V  V  V  T   100

301 GGGCGGGAGCCAGACAGCCGTCGTCAGGACGGTGCCATGTCCAGCTCTGACGCCGAAGAC  360
101 G  R  E  P  D  S  R  R  Q  D  G  A  M  S  S  S  D  A  E  D   120

361 GACTTTCTGGAGCCGGCCACGCCGACGGCCACGCAGGCGGGGCACGCGCTGCCCCTGCTG  420
121 D  F  L  E  P  A  T  P  T  A  T  Q  A  G  H  A  L  P  L  L   140

421 CCACAGGAGTTTCCTGAGGTTGTTCCCCTTAACATCGGAGGGGCTCACTTCACTACACGC  480
141 P  Q  E  F  P  E  V  V  P  L  N  I  G  G  A  H  F  T  T  R   160

481 CTGTCCACACTGCGGTGCTACGAAGACACCATGTTGGCAGCCATGTTCAGTGGGCGGCAC  540
161 L  S  T  L  R  C  Y  E  D  T  M  L  A  A  M  F  S  G  R  H   180

541 TACATCCCCACAGACTCCGAGGGCCGGTACTTCATCGACCGAGATGGCACACACTTTGGA  600
181 Y  I  P  T  D  S  E  G  R  Y  F  I  D  R  D  G  T  H  F  G   200

601 GATGTGCTGAATTTCCTGCGCTCAGGGGACCTCCCACCCAGGGAGCGTGTTCGAGCTGTG  660
201 D  V  L  N  F  L  R  S  G  D  L  P  P  R  E  R  V  R  A  V   220

661 TACAAAGAGGCCCAGTACTATGCCATCGGGCCCCTCCTGGAGCAGCTGGAGAACATGCAG  720
221 Y  K  E  A  Q  Y  Y  A  I  G  P  L  L  E  Q  L  E  N  M  Q   240

721 CCACTGAAGGGCGAGAAGGTGCGCCAAGCGTTTCTGGGACTCATGCCCTATTACAAAGAC  780
241 P  L  K  G  E  K  V  R  Q  A  F  L  G  L  M  P  Y  Y  K  D   260

781 CACTTGGAGCGGATTGTGGAGATCGCCCGGCTGCGTGCGGTCCAGCGGAAGGCCCGCTTT  840
261 H  L  E  R  I  V  E  I  A  R  L  R  A  V  Q  R  K  A  R  F   280
```

Figure 6B

```
841  GCCAAGCTCAAGAGCTTGACACCTTCCTGGCTAATGAGTGTCCTCATCAAGATGCCCCCT  900
281  A  K  L  K  S  L  T  P  S  W  L  M  S  V  L  I  K  M  P  P    300

901  GGAGTCACATCATGGATTAACGCAGAAAGGCGGCTGTATTTGGAAACTCCCATTGGTCCA  960
301  G  V  T  S  W  I  N  A  E  R  R  L  Y  L  E  T  P  I  G  P    320

961  GAGAGACAGAACAATGAGAAGAAATCCCCTGTCCAGTTGCCTGCAGGAGTATTCCAACAC  1020
321  E  R  Q  N  N  E  K  K  S  P  V  Q  L  P  A  G  V  F  Q  H    340

1021 TTCATGGGCTAGAGGATTCCATTGAGATGGGGTTTACGTCTTGATTTTGAACACCTGTCA  1080
341  F  M  G                                                       343

1081 GCACTGTTCTCTGTTTGCATGGCAATTCTGACCCTTTTATGGCAACAACACCCCTGGGAC  1140

1141 AACCCAGATTTGTAGATTGAGATCCAAAGGTAGAATTTCCAGACAGTCCAACCAAGGTAT  1200

1201 CAAGTGATGTTTCCAGAGTGGAAGGCTCTCACCGTGTCCCAGGATTTCTGGGGTTTGTAA  1260

1261 GCAGTACTGGCCATTTGTGACCCTGTTTTTTACCTAATCATTCTGTCTTTTTAGGACATG  1320

1321 GTTTTACCCGATCCCTGGCAAAGGATCCAGAATTCCAATAGCTGAAAACCCTGTTATAGC  1380

1381 TTTTCTCCTATTCTGCCTTACCCAAGACACACTTGAACCCCTCAGTAAGGCTATAGAGAG  1440

1441 GGCCATGAGCAGGGGCAGCCTCTCCCTTGTTTCTACAGCTCCATGATGAGGGGTTGACTG  1500

1501 AGGCCAGCAATCCTTGTAGGTGTGACAGTTGCAATATAATTAACAGTTTCAAGATCTAGA  1560

1561 GGTACCTTTTGAAAGAACCCCTTCAGGGATATCTATCCACAGTAGCCTGGAGCAGCCAAG  1620

1621 GTGAACCTGAGATTTTGACCCACACAATAAGGGGGGGCCATTCTTTTTCAAATATTTTGG  1680

1681 CTTCAGAATACACTTCATTACACATGCAAATATTGAGAGATTAACAGAAATTCCAGCTCT  1740

1741 TATGCCTAACTGAGAAGAGCCACTGCAAGTTGCAGTTAGGTACCCATGTGCAGCAGAGGC  1800

1801 CAGCTGAATCCCAGAGCTTCCCAAAGTGGACACCAGCGGGGACTATTCCTGATGTCCCAC  1860

1861 CCAAGAGAGGAAGATGAGCTGAGGCGCTCTTGCTCTGCCCAAATGCATCCCATGTGCATT  1920
```

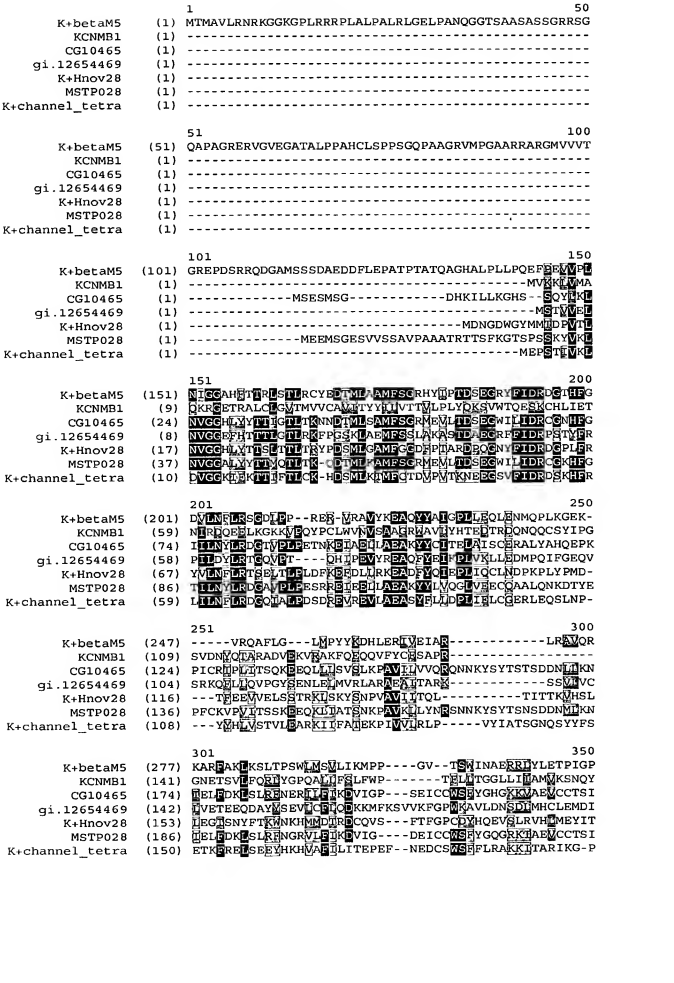
D0115 NP

Figure 6C

```
1921  CACGTGTCACCCATTCAAAATAACATGGCATTCTTGGAACCTTGTATCTGACATGTAAGA  1980

1981  CCAGCCTACACATTGGGGTGGGTGCAGGGGCTCACACTTGTAATCCTAGCACTTTGGAAG  2040

2041  GCTGAGGTGGGCAGATTGCTTGAGCACAGGAGTTCCAGACCAGCCTGAGCAACATGGCGA  2100

2101  AATCCTGTCTCTTCAAGAAATAAAATAATAATAATAAAAAAAAAAAAAAAA  2154
```

D0115 NP

Figure 7A



D0115 NP

Figure 7B

```
                      351                                                 400
        K+betaM5  (321) ERQNNEKKEPVQLPAGVFQHFMG--------------------------
          KCNMB1  (184) DSILAAQK-----------------------------------------
          CG10465 (221) MYATDRSHHKVEFPEEANIYEETLQVLLYENRN--APDQELMQATSSARVG
     gi.12654469  (192) KAQGYKVFSKFYLTYPTKRNEFHFNIYSFTFTWW----------------
          K+Hnov28 (200) KQGFTINNTRVHHMSERANENTVEHNWTFCRLARKTDD-------------
          MSTP028  (232) MYATEKKQTKVEFPEEANIYEETLNILLYEAQDGRGPDNALLEATG-----
  K+channel_tetra  (197) MDCNLVEECMPKTVERREKKTWH--------------------------

                      401                                         440
        K+betaM5  (344) ------------------------------------------
          KCNMB1  (192) ------------------------------------------
          CG10465 (269) SASGTSINQYTSDEEEERTGLARLRSNKRNNPS-------
     gi.12654469  (226) ------------------------------------------
          K+Hnov28 (238) ------------------------------------------
          MSTP028  (277) ---GAAGRSHHLDEDEERERIERVRRIHIKRPDDRAHLHQ
  K+channel_tetra  (221) ------------------------------------------
```

D0115 NP

Figure 8

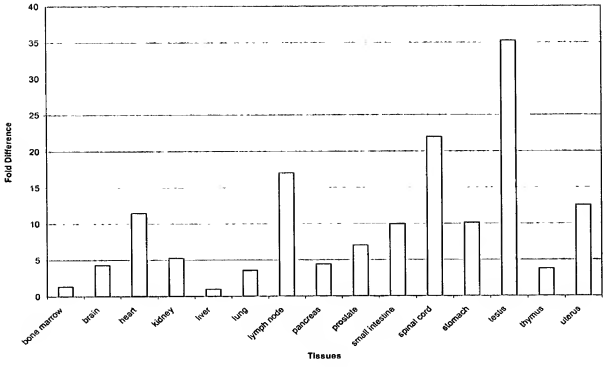


Figure 9